

SEQUENCE LISTING

<110> NeuTec Pharma plc

<120> Medicament

<130> M99/0035/PCT

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<150> GB9902555.3

<151> 1999-02-05

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 1491

<212> DNA

<213> Chlamydia pneumoniae

<220>

<221> CDS

<222> (1)..(1491)

<400> 1

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aat	atc	atg	tct	caa	gtt	ctg	aca	tgc	aca	ccc	cag	ggc	gtg	ccc	caa	96
Asn	Ile	Met	Ser	Gln	Val	Leu	Thr	Ser	Thr	Pro	Gln	Gly	Val	Pro	Gln	
20					25								30			

caa	gat	aag	ctg	tct	ggc	aac	gaa	acg	aag	caa	ata	cag	caa	aca	cgt	144
Gln	Asp	Lys	Leu	Ser	Gly	Asn	Glu	Thr	Lys	Gln	Ile	Gln	Gln	Thr	Arg	
35					40								45			

cag	ggt	aaa	aac	act	gag	atg	gaa	agc	gat	gcc	act	att	gct	ggt	gct	192
Gln	Gly	Lys	Asn	Thr	Glu	Met	Glu	Ser	Asp	Ala	Thr	Ile	Ala	Gly	Ala	
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tct	gga	aaa	gac	aaa	act	tcc	tgc	act	aca	aaa	aca	gaa	aca	gct	cca	240
Ser	Gly	Lys	Asp	Lys	Thr	Ser	Ser	Thr	Thr	Lys	Thr	Glu	Thr	Ala	Pro	
65					70								75		80	

caa	cag	gga	gtt	gct	gct	ggg	aaa	gaa	tcc	tca	gaa	agt	caa	aag	gca	288
Gln	Gln	Gly	Val	Ala	Ala	Gly	Lys	Glu	Ser	Ser	Glu	Ser	Gln	Lys	Ala	
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ggt	gct	gat	act	gga	gta	tca	gga	gct	gct	act	aca	gca	tca	aat	336
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Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn			
100	105	110	
act gca aca aaa att gct atg cag acc tct att gaa gag gcg agc aaa		384	
Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys			
115	120	125	
agt atg gag tct acc tta gag tca ctt caa agc ctc agt gcc gcg caa		432	
Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln			
130	135	140	
atg aaa gaa gtc gaa gcg gtt gtt gct gcc ctc tca ggg aaa agt		480	
Met Lys Glu Val Glu Ala Val Val Ala Ala Leu Ser Gly Lys Ser			
145	150	155	160
tcg ggt tcc gca aaa ttg gaa aca cct gag ctc ccc aag ccc ggg gtg		528	
Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val			
165	170	175	
aca cca aga tca gag gtt atc gaa atc gga ctc gcg ctt gct aaa gca		576	
Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala			
180	185	190	
att cag aca ttg gga gaa gcc aca aaa tct gcc tta tct aac tat gca		624	
Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala			
195	200	205	
agt aca caa gca caa gca gac caa aca aat aaa cta ggt cta gaa aag		672	
Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys			
210	215	220	
caa gcg ata aaa atc gat aaa gaa cga gaa gaa tac caa gag atg aag		720	
Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys			
225	230	235	240
gct gcc gaa cag aag tct aaa gat ctc gaa gga aca atg gat act gtc		768	
Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val			
245	250	255	
aat act gtg atg atc gcg gtt tct gtt gcc att aca gtt att tct att		816	
Asn Thr Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile			
260	265	270	
gtt gct gct att ttt aca tgc gga gct gga ctc gct gga ctc gct gcg		864	
Val Ala Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala			
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gga gct gct gta ggt gca gcg gca gct gga ggt gca gca gga gct gct		912	
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gcc gca acc acg gta gca aca caa att aca gtt caa gct gtt gtc caa		960	
Ala Ala Thr Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln			

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305	310	315	320	
gct gtc aaa caa gct gtt atc aca gct gtc aga caa gct atc acc acc				1008
Ala Val Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala				
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gct ata aaa gct gtc aaa tct gga ata aaa gca ttt atc aaa act				1056
Ala Ile Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr				
340	345	350		
tta gtc aaa gct att gcc aaa gcc att tct aaa gga atc tct aag gtt				1104
Leu Val Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val				
355	360	365		
ttc gct aag gga act caa atg att gct aag aac ttc ccc aag ctc tcg				1152
Phe Ala Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser				
370	375	380		
aaa gtc atc tcg tct ctt acc agt aaa tgg gtc acg gtt ggg gtt ggg				1200
Lys Val Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly				
385	390	395	400	
gtt gta gtt gcg gcg cct gct ctc ggt aaa ggg att atg caa atg cag				1248
Val Val Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln				
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ctc tcg gag atg caa caa aac gtc gct caa ttt cag aaa gaa gtc gga				1296
Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly				
420	425	430		
aaa ctg cag gct gcg gct gat atg att tct atg ttc act caa ttt tgg				1344
Lys Leu Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp				
435	440	445		
caa cag gca agt aaa att gcc tca aaa caa aca ggc gag tct aat gaa				1392
Gln Gln Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu				
450	455	460		
atg act caa aaa gct acc aag ctg ggc gct caa atc ctt aaa gct tat				1440
Met Thr Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr				
465	470	475	480	
gcc gca atc agc gga gcc atc gct ggc gca cat aaa acc aat aat ttt				1488
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taa				1491

<210> 2
<211> 496
<212> PRT

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<213> Chlamydia pneumoniae

<400> 2

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Gln	Asp	Lys	Leu	Ser	Gly	Asn	Glu	Thr	Lys	Gln	Ile	Gln	Gln	Thr	Arg
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Gln	Gly	Lys	Asn	Thr	Glu	Met	Glu	Ser	Asp	Ala	Thr	Ile	Ala	Gly	Ala
					50			55			60				
Ser	Gly	Lys	Asp	Lys	Thr	Ser	Ser	Thr	Thr	Lys	Thr	Glu	Thr	Ala	Pro
					65			70			75		80		
Gln	Gln	Gly	Val	Ala	Ala	Gly	Lys	Glu	Ser	Ser	Glu	Ser	Gln	Lys	Ala
					85			90			95				
Gly	Ala	Asp	Thr	Gly	Val	Ser	Gly	Ala	Ala	Ala	Thr	Thr	Ala	Ser	Asn
					100			105			110				
Thr	Ala	Thr	Lys	Ile	Ala	Met	Gln	Thr	Ser	Ile	Glu	Glu	Ala	Ser	Lys
					115			120			125				
Ser	Met	Glu	Ser	Thr	Leu	Glu	Ser	Leu	Gln	Ser	Leu	Ser	Ala	Ala	Gln
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Met	Lys	Glu	Val	Glu	Ala	Val	Val	Ala	Ala	Leu	Ser	Gly	Lys	Ser	
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Ser	Gly	Ser	Ala	Lys	Leu	Glu	Thr	Pro	Glu	Ieu	Pro	Lys	Pro	Gly	Val
					165			170			175				
Thr	Pro	Arg	Ser	Glu	Val	Ile	Glu	Ile	Gly	Leu	Ala	Leu	Ala	Lys	Ala
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Ile	Gln	Thr	Leu	Gly	Glu	Ala	Thr	Lys	Ser	Ala	Leu	Ser	Asn	Tyr	Ala
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Ser	Thr	Gln	Ala	Gln	Ala	Asp	Gln	Thr	Asn	Lys	Leu	Gly	Leu	Glu	Lys
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Gln	Ala	Ile	Lys	Ile	Asp	Lys	Glu	Arg	Glu	Glu	Tyr	Gln	Glu	Met	Lys
					225			230			235		240		
Ala	Ala	Glu	Gln	Lys	Ser	Lys	Asp	Leu	Glu	Gly	Thr	Met	Asp	Thr	Val
					245			250			255				
Asn	Thr	Val	Met	Ile	Ala	Val	Ser	Val	Ala	Ile	Thr	Val	Ile	Ser	Ile
					260			265			270				
Val	Ala	Ala	Ile	Phe	Thr	Cys	Gly	Ala	Gly	Leu	Ala	Gly	Leu	Ala	Ala
					275			280			285				
Gly	Ala	Ala	Val	Gly	Ala	Ala	Ala	Gly	Gly	Ala	Ala	Gly	Ala	Ala	
					290			295			300				
Ala	Ala	Thr	Thr	Val	Ala	Thr	Gln	Ile	Thr	Val	Gln	Ala	Val	Val	Gln
					305			310			315		320		
Ala	Val	Lys	Gln	Ala	Val	Ile	Thr	Ala	Val	Arg	Gln	Ala	Ile	Thr	Ala
					325			330			335				
Ala	Ile	Lys	Ala	Ala	Val	Lys	Ser	Gly	Ile	Lys	Ala	Phe	Ile	Lys	Thr
					340			345			350				
Leu	Val	Lys	Ala	Ile	Ala	Lys	Ala	Ile	Ser	Lys	Gly	Ile	Ser	Lys	Val
					355			360			365				
Phe	Ala	Lys	Gly	Thr	Gln	Met	Ile	Ala	Lys	Asn	Phe	Pro	Lys	Leu	Ser
					370			375			380				
Lys	Val	Ile	Ser	Ser	Leu	Thr	Ser	Lys	Trp	Val	Thr	Val	Gly	Val	Gly
					385			390			395		400		

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Val Val Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln
405 410 415
Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly
420 425 430
Lys Leu Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp
435 440 445
Gln Gln Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu
450 455 460
Met Thr Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr
465 470 475 480
Ala Ala Ile Ser Gly Ala Ile Ala Gly Ala His Lys Thr Asn Asn Phe
485 490 495

<210> 3

<211> 302

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Codon optimised N-terminal section of Chlamydia pneumoniae protein

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<221> UNSURE

<222> (1)..(30)

<223> S-tag and thrombin cleavage site

<220>

<221> UNSURE

<222> (292)..(302)

<223> Histidine tag

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Asp Thr Asn Met Ser Ile Ser Ser Ser Gly Pro Asp Asn Gln Lys
35 40 45

Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln
50 55 60

Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg
65 70 75 80

Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala
85 90 95

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Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro
100 105 110

Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala
115 120 125

Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn
130 135 140

Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys
145 150 155 160

Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln
165 170 175

Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser
180 185 190

Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val
195 200 205

Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala
210 215 220

Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala
225 230 235 240

Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys
245 250 255

Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys
260 265 270

Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val
275 280 285

Asn Thr Val Ala Ala Ala Leu Glu His His His His His His
290 295 300

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<212> PRT

<213> Chlamydia pneumoniae

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Ser Ala Lys Leu Glu Thr Pro Glu Leu
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<210> 5

<211> 7

<212> PRT

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<213> Chlamydia pneumoniae

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<210> 6
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<210> 16
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<213> Chlamydia pneumoniae

<400> 16
Glu Thr Pro Glu Leu Pro Lys Pro Gly Val Thr Pro Arg Ser
1 5 10

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